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Group Art Unit: 1638

REMARKS

Reconsideration of the present application is respectfully requested. Claims 1, and 3-9 are pending. Claims 2, and 10-13 have been cancelled as belonging to a non-elected invention. The right to pursue these claims in a continuing application is reserved. No change of inventorship is necessary. Claims 1, 3, and 5 have been amended. Support for the amendments is found in the claims as originally filed, and throughout the specification. No new matter has been added.

Applicant has amended the specification to delete references to Internet hyperlinks.

The marked up version of these amendments is found on a separate sheet attached to this amendment and titled **"Version with Markings to Show Changes Made."** It is respectfully requested that the amendments be entered.

Election/Restriction

The Examiner has issued a restriction requirement, and has required election of either the invention of Group I (Claims 1-9) or Group II (Claims 10-12) or Group III (Claim 13). Applicants hereby affirm the election to prosecute the claims of Group I, with traverse as filed 8/31/01.

A supplemental election was made over the telephone on 10/6/01 to prosecute SEQ ID NO: 3 encoding SEQ ID NO: 4, Group I (Claims 1, and 3-9). This supplemental election is affirmed, with traverse. As presented in Appendix A, the sequences of the present invention show a high degree of homology to each other. Sequence election is at the discretion of the Examiner, the MPEP allows up to 10 sequences to be examined together. As the searches for these sequences likely overlap, Applicants respectfully request the sequences, or a subset of the sequences, to be rejoined with SEQ ID NO: 3 encoding SEQ ID NO: 4.

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Applicants expressly reserve the right to file a divisional applications relating to and claiming the inventions of Group II and/or Group III. No change of inventorship is required due to this election of Group I, SEQ ID NO: 3 encoding SEQ ID NO: 4.

Rejections under 35 U.S.C. §112, 2nd Paragraph:

Claims 3-9 are rejected under 35 U.S.C. §112, second paragraph, as being indefinite.

The Examiner asserts claim 3 is an improper multiple dependent claim.

Claim 3 has been amended, and now depends only from claim 1. The rejection under 35 U.S.C. §112, second paragraph no longer applies.

The Examiner asserts claim 5, "a" should be "the" in reference to the recombinant expression cassette.

Claim 5 has been amended to read "the recombinant expression cassette" as recommended by the Examiner.

Applicants have addressed the rejection under 35 U.S.C. §112, second paragraph by proper amendments to the claims. Therefore, Applicants respectfully request the rejection of claims 3-9 under 35 U.S.C. §112, second paragraph be withdrawn.

Rejections under 35 U.S.C. §101:

Claims 1, 3-9 are rejected under 35 U.S.C. §101 as not having either a credible asserted utility or a well-established utility.

The Examiner asserts that "No function of said polynucleotides are recited."

Applicants have amended claim 1, which now recites "wherein the polynucleotide encodes a polypeptide with RuvB activity." Therefore, as amended claim 1 and dependent claims 3-9 do recite the function of the polynucleotides.

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The Examiner asserts "Applicants assert that a polynucleotide having 85% sequence identity to SEQ ID NO: 1 would have RuvB activity. However it is unclear what would be the utility of said polynucleotide if the 15% lack of identity falls in a region crucial for the RuvB activity."

Applicants have amended claim 1. In the preamble, Claim 1 recites "An isolated polynucleotide encoding a polypeptide with RuvB activity ". Therefore, only polynucleotides with 85% sequence identity to SEQ ID NO: 1, which also encode a polypeptide with RuvB activity are claimed. Further, not all embodiments must have utility for the invention as a whole to have utility. Inoperable embodiments of the claimed invention do not eliminate the utility of the operable embodiments. As it is stated in the MPEP 2107 II, page 2100-25: "... as the Federal Circuit has stated, '[t]o violate [35 U.S.C.] 101 the claimed device must be totally incapable of achieving a useful result.' *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571, 24 USPQ2d 1401, 1412 (Fed. Cir. 1992)".

The Examiner states "No data that relates SEQ ID NO: 3 or SEQ ID NO: 4 to RuvB activity has been shown."

Applicants respectfully disagree, page 2, lines 13-26 and Example 4 on pages 63-64 of the specification clearly detail the well-established activity and features of RuvB polypeptides. RuvB has been shown to be involved in DNA recombination, the present invention proposes to use the well established activity of RuvB to improve transformation efficiency in plants, therefore establishing specific and substantial utility for the present invention. Page 2, lines 13-26, and in Example 4 on pages 63-64, of the specification discuss the structural features shared by SEQ ID NO:4 of the present invention and other known RuvB proteins, including the presence of two ATP-binding sites (Walker boxes), heptad repeats, and regions conserved in bacterial RuvB proteins. In Appendix A, Applicants submit a multiple sequence alignment of SEQ ID NO: 4 with several other RuvB proteins. Identical and conserved amino acids, relative to SEQ ID NO: 4, are highlighted. The multiple

sequence alignment illustrates the extensive homology, over the entire length of SEQ ID NO: 4, to other RuvB proteins.

The Examiner asserts "However, the state of the art as exemplified by Bork et al suggests sequence identity is insufficient to predictably determine a protein function."

The identification of SEQ ID NO: 3 and SEQ ID NO: 4 as RuvB polynucleotide and polypeptide respectively, is not based merely on percent sequence identity alone, but is based on an analysis of several features, such as molecular weight, and sequence homology to known conserved domains contained in RuvB. These features include the presence and positioning of ATP-binding sites, heptad repeats, and conserved domains in bacterial RuvB polypeptides (see Example 4). As illustrated in the multiple sequence alignment presented in Appendix A, there is substantial homology to other RuvB proteins across the entire length of SEQ ID NO: 4. Therefore, the Applicant has established a credible utility for the sequences of the present invention.

While Bork (Genome Research 10:398-400, 2000) certainly wishes to warn about the potential limits to extrapolating the data of high-throughput technologies which automatically annotate genomic sequencing efforts, he does not state that computer-based homology searches are invalid or questionable. In fact, on page 400, second column, second paragraph Bork states " However there is still no doubt that sequence analysis is extremely powerful and that the generation of hypotheses derived by computational methods will be more and more often the first successful step in the design of experiments. If 70% of such experiments were successful, the speed of scientific discoveries would grow exponentially."

The Applicants also respectfully draw the Examiner's attention to the Utility Examination Guidelines, Official Gazette, January 30, 2001 which state "... when a patent application claiming a nucleic acid asserts a specific, substantial, and credible utility, and bases the assertion upon homology to existing nucleic acids having an

accepted utility, the asserted utility must be accepted by the examiner unless the Office has sufficient evidence or sound scientific reasoning to rebut such an assertion." The Guidelines further state "[A] 'rigorous correlation' need not be shown in order to establish practical utility; 'reasonable correlation' is sufficient." *Fujikawa v. Wattanasin*, 93 F.3d 1559, 1565, 39 USPQ2d 1895, 1900 (Fed. Cir. 1996).

Applicants believe that the present invention has a well-established utility for which they have proposed specific, substantial and credible uses in the present application. Applicants have properly addressed by argument and amendment the grounds for the rejection of originally filed claims 1-18 under 35 U.S.C. §101 as it would apply to pending claims 2-8, and 12-15, and respectfully request that the rejection of the claims under 35 U.S.C §101 be withdrawn.

Rejections under 35 U.S.C. §112, first paragraph – Utility:

As the Applicants have responded to the utility rejection under 35 U.S.C. §101, the concomitant rejection of claims 1, and 3-9 under 35 U.S.C. §112, first paragraph based on a lack of utility should be withdrawn.

Rejections under 35 U.S.C. § 102:

Claims 1, and 3-9 have been rejected under 35 U.S.C. § 102(b) as being anticipated by Boudet et al. (US Patent 5,451,514).

The Examiner asserts "The claims read on a polynucleotide with 2-bases, since any two bases would hybridize and would be complementary to the claimed polynucleotide."

Claim 1 was amended, claim 1, part (d) now recites "a polynucleotide which is fully complementary to a polynucleotide of (a), (b) or (c)".

The Applicants respectfully disagree that the claims encompass 2 nucleotide fragments. Sequences of only two nucleotides in length would not even **anneal** to the nucleic acid of the present invention under most conditions, much less

selectively hybridize to the nucleic acid of the present invention as it is defined on page 14, line 30 – page 15, line 3 under **stringent conditions** as described on pages 14, line 24 – page 16, line 11 of the specification. Using the quick calculation for melting temperature (Tm) of 4° C for every G or C nucleotide, or 2° C for every A or T nucleotide (Wallace formula), one can quickly calculate the approximate maximum Tm for a two nucleotide sequence to be 8° C, annealing temperature is generally calculated as 5° C lower than the Tm, or 3° C in this case. It is apparent that subsequences of only 2 nucleotides in length are not capable of annealing to, much less selectively hybridizing with, the nucleic acid of the present invention, therefore the rejection of claim 1 (d) should be withdrawn.

The Applicants respectfully traverse the rejection under 35 U.S.C. § 102(b). As it is stated in the MPEP 2131 page 2100-54 "To anticipate a claim, the reference must teach every element of the claim. 'A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference.'"

Boudet *et al.* do not disclose a polynucleotide having 85% sequence identity over the entire coding region of SEQ ID NO: 3, or a polynucleotide which encodes a polypeptide with RuvB activity, or a polynucleotide which is fully complementary to a polynucleotide which encodes a polypeptide with RuvB activity. Therefore, Boudet *et al.* does not anticipate the claims and the rejection under 35 U.S.C. § 102(b) should be withdrawn.

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CONCLUSION

In light of the foregoing remarks and amendments, withdrawal of the outstanding rejections and allowance of all of the remaining claims is respectfully requested.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

The Applicants have used underlining to denote additions to the original text and square brackets [ ] to denote deletions of the original text.

In the Title:

The title found on the cover page has been amended as follows:

[Maize Orthologues of Bacterial] RuvB[: cDNA] Orthologues and Uses Thereof

In the Specification:

Paragraph beginning at line 3 of page 18 has been amended as follows:

Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information [(http://www.ncbi.nlm.nih.gov/)]. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of

the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

Paragraph beginning at line 29 of page 62 has been amended as follows:

Gene identities were determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1990) J. Mol. Biol. 215:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]) searches under default parameters for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm. The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. Nature Genetics 3:266-272 (1993)) provided by the NCBI. In some cases, the sequencing data from two or more clones containing overlapping segments of DNA were used to construct contiguous DNA sequences.

The Abstract beginning at line 1 of page 68 has been amended as follows:

ABSTRACT OF THE DISCLOSURE

The invention provides isolated [maize] RuvB nucleic acids and their encoded proteins. The present invention provides methods and compositions relating to altering [maize] RuvB levels in plants. The invention further provides recombinant expression cassettes, host cells, transgenic plants, and antibody compositions.

In the Claims:

Claims 2 and 10-13 have been cancelled without prejudice.

Claims 1, 3 and 5 have been amended as follows:

1. (Amended) An isolated nucleic acid comprising a member selected from the group consisting of:
   (a) a polynucleotide having at least 85% sequence identity to a polynucleotide [selected from the group consisting] of SEQ ID NO[S]: [1,] 3[, and 9], wherein the % sequence identity is based on the entire coding region[s] and is calculated by the GAP algorithm under default parameters, wherein the polynucleotide encodes a polypeptide with RuvB activity;
   (b) a polynucleotide encoding a polypeptide [selected from the group consisting] of SEQ ID NO[S]: [2,] 4[, and 10];
   (c) a polynucleotide [selected from the group consisting] of SEQ ID NO[S]: [1,] 3[, and 9]; and
   (d) a polynucleotide which is fully complementary to a polynucleotide of (a), (b), or (c).

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3. (Amended) A recombinant expression cassette, comprising a polynucleotide of claim 1 operably linked[, in sense or anti-sense orientation,] to a promoter[, wherein said polynucleotide is selected from the group consisting of a member of claim 1 and a member of claim 2].

5. (Amended) A transgenic plant comprising [a] the recombinant expression cassette of claim 3.

APPENDIX A

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AF070735aa	Human RuvB protein encoded by GenBank AF070735
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1121SID8	Maize RuvB Case 1121 SEQ ID NO: 8
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1121SID4	**Maize RuvB Case 1121 SEQ ID NO: 4**
1121SID10	Maize RuvB Case 1121 SEQ ID NO: 10
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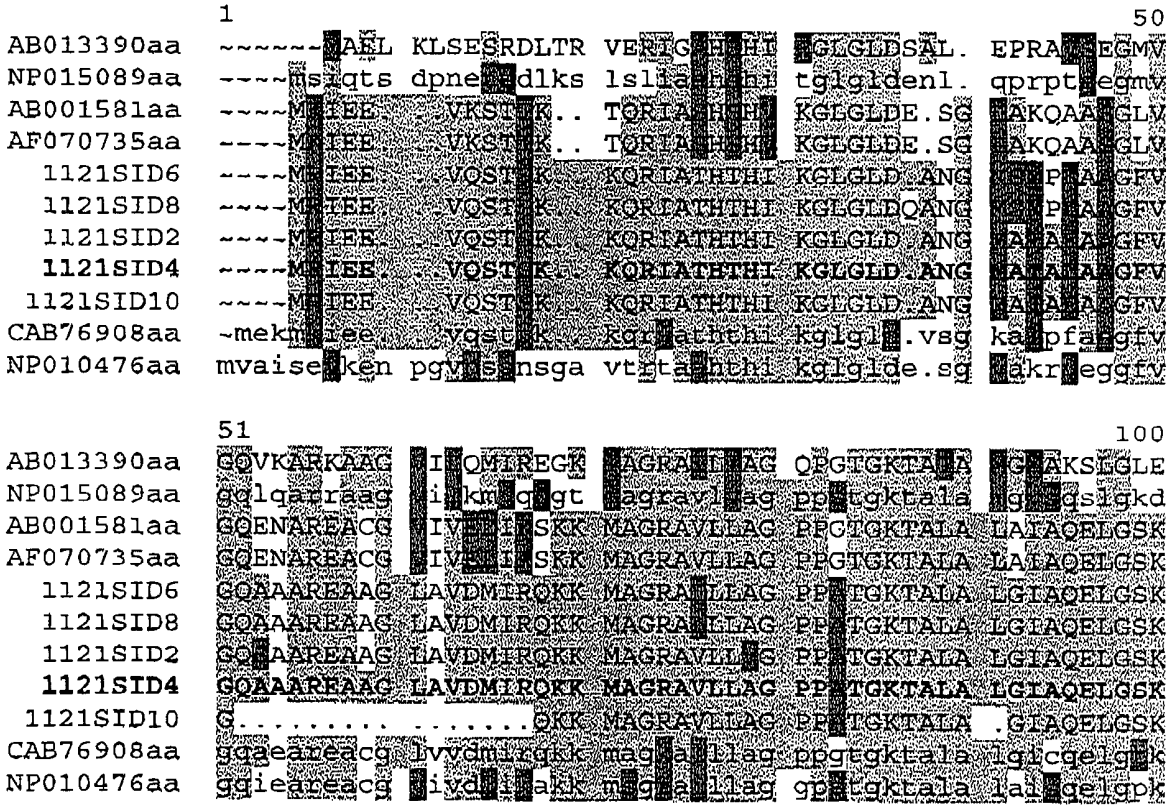
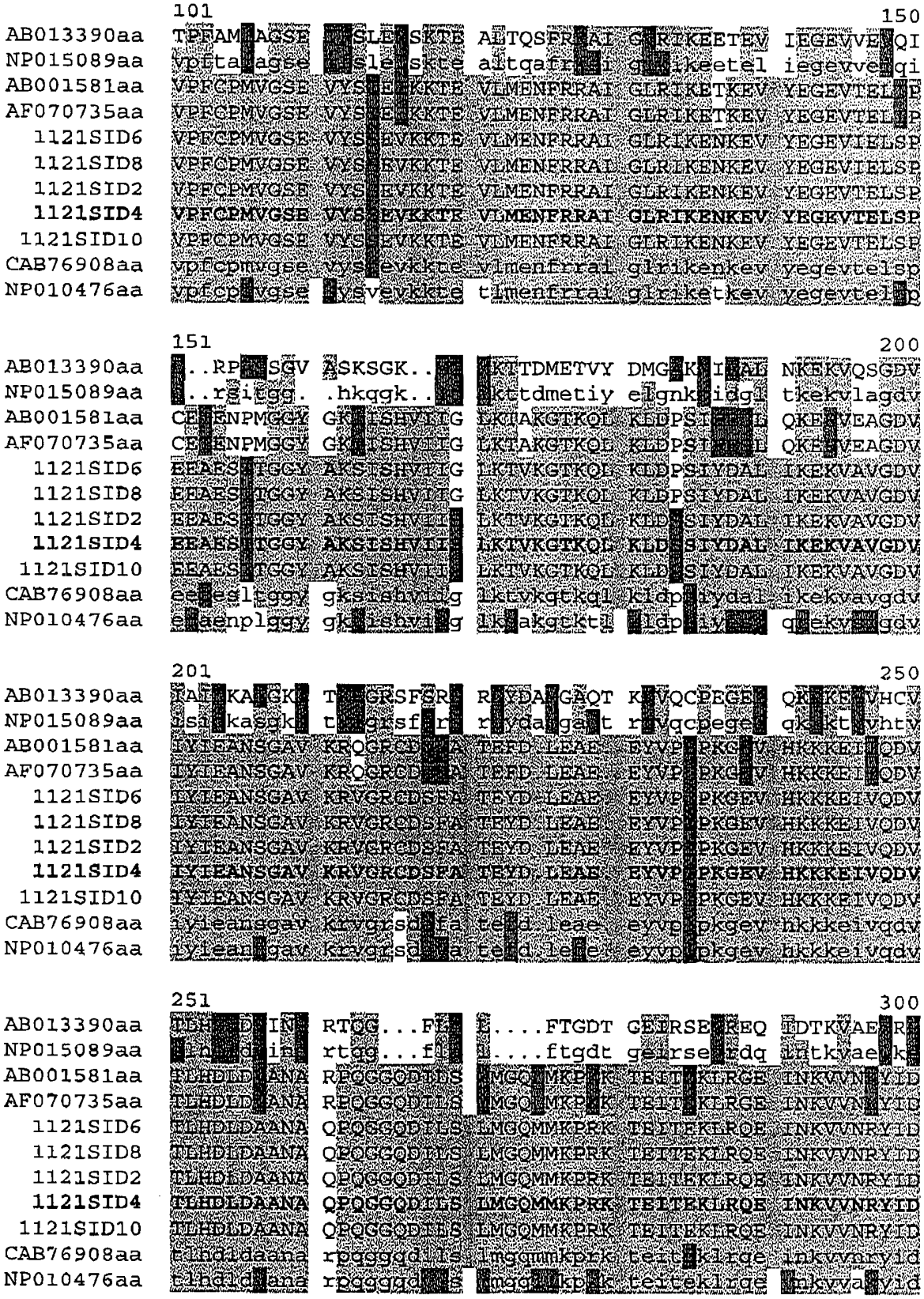
Residue [redacted] to SEQ ID NO: 4

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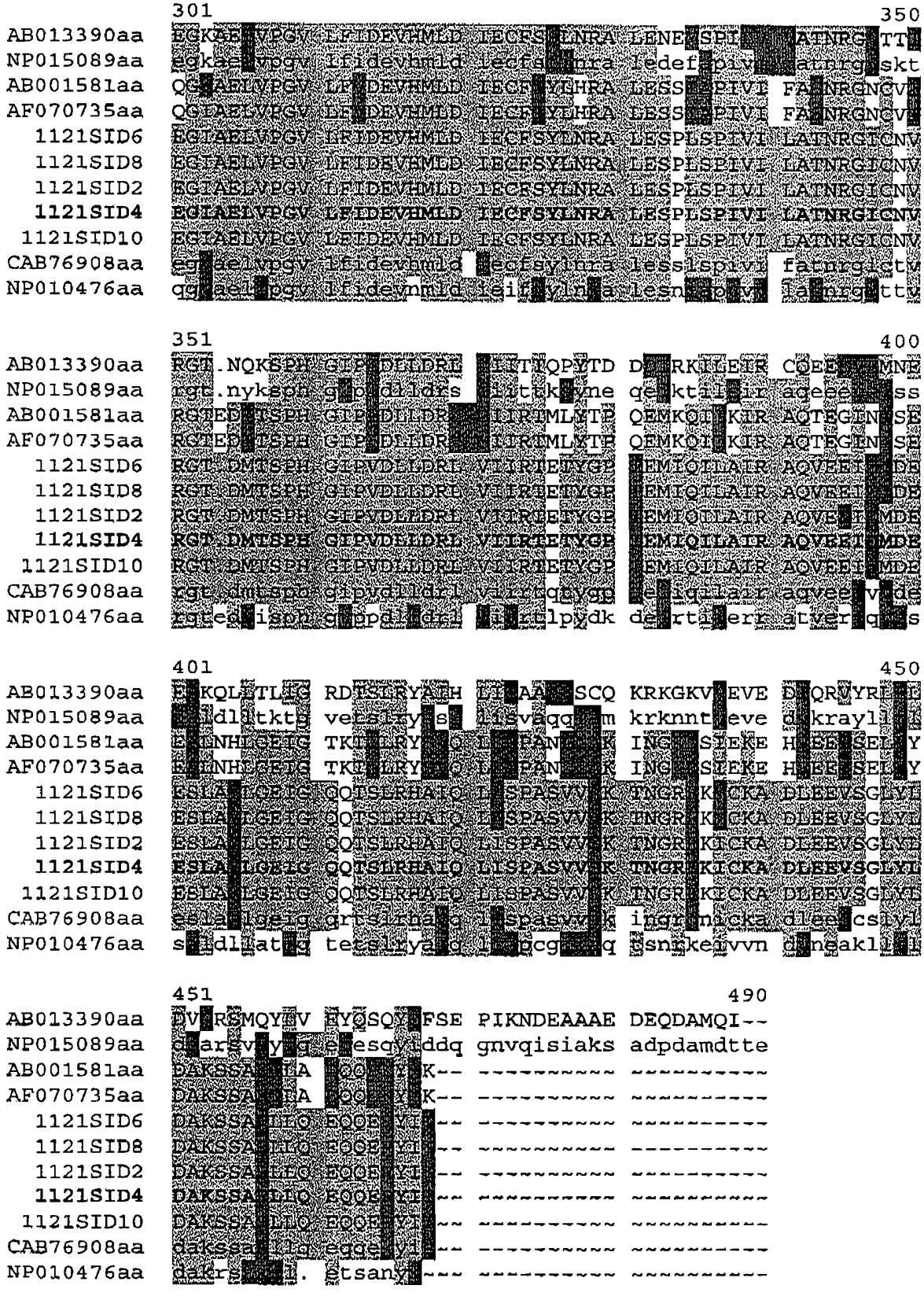
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  TITLE     An eukaryotic RuvB-like protein (RUVBL1) essential for growth
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  AUTHORS   Qiu,X.-B., Lin,Y.-L., Thome,K.C., Pian,P., Schlegel,B.P.,
            Weremowicz,S., Parvin,J.D. and Dutta,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1998) Pathology, Brigham & Women's Hospital,
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Revised: October 24, 2001.

NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Books

Search Nucleotide for Go Clear

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  AUTHORS   Kikuchi,N., Gohshi,T., Kawahire,S., Tachibana,T., Yoneda,Y.,
            Isobe,T., Lim,C.R., Kohno,K., Ichimura,T., Omata,S. and Horigome,T.
  TITLE     Molecular shape and ATP binding activity of rat p50, a putative
            mammalian homologue of RuvB DNA helicase
  JOURNAL   J. Biochem. 125 (3), 487-494 (1999)
  MEDLINE   99160601
REFERENCE   2  (bases 1 to 1567)
  AUTHORS   Kikuchi,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1997) Noriko Kikuchi, Niigata University,
            Department of Chemistry, Faculty of Science; Igarashi-2, Niigata,
            Niigata 950-21, Japan (E-mail:tenten@rtc.riken.go.jp,
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   1441 cttgcgttga cgatgctttc gagtgttaca gtttgttttgt aaattatcaa acctccaagg
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Revised: October 24, 2001.

1: CAB76908. putative Ruv DNA-...[gi:7208771] Nucleotide, Related Sequences, Taxonomy, BLink, LinkOut

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DEFINITION  putative Ruv DNA-helicase [Cicer arietinum].
ACCESSION   CAB76908
PID         g7208771
VERSION     CAB76908.1  GI:7208771
DBSOURCE    embl locus CAR276264, accession AJ276264.1
KEYWORDS    .
SOURCE      chickpea.
  ORGANISM  Cicer arietinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae;
            Cicer.
REFERENCE   1  (residues 1 to 458)
  AUTHORS   Dopico,B., Esteban,R. and Labrador,E.
  TITLE     A RuvB DNA-helicase like protein is expressed in chickpea epicotyls
  JOURNAL   Unpublished
REFERENCE   2  (residues 1 to 458)
  AUTHORS   Labrador,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-FEB-2000) Labrador E., Dpto. Fisiologia Vegetal,
            Univ. Salamanca, Campus Miguel de Unamuno. Pza. Doctores de la
            Reina s/n, E-37007, SPAIN
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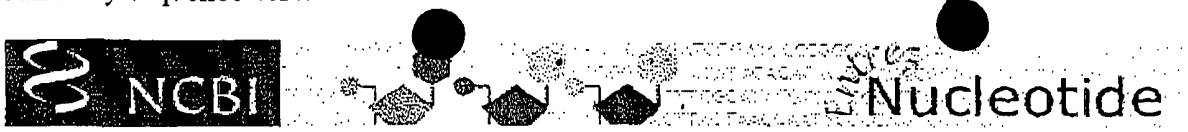

FASTA view

Sequence feature view of the region: (gi|3128137:c48472-47724, c47361-46701)

AB013390.1 CDS for K9I9.20

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DEFINITION CDS from: Arabidopsis thaliana genomic DNA, chromosome 5, TA clone:K9I9.
ACCESSION 3128137
VERSION 3128137
KEYWORDS .
SOURCE Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui clone:K9I9.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
REFERENCE 1 (sites)
AUTHORS Kotani,H., Nakamura,Y., Sato,S., Asamizu,E., Kaneko,T., Miya and Tabata,S.
TITLE Structural analysis of Arabidopsis thaliana chromosome 5. VI Sequence features of the regions of 1,367,185 bp covered by physically assigned P1 and TAC clones
JOURNAL DNA Res. 5 (3), 203-216 (1998)
MEDLINE 98403884
REFERENCE 2 (bases 46701 to 48472)
AUTHORS Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-1998) Yasukazu Nakamura, Kazusa DNA Resear Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, plea http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=K9I9
Genes with similarity to proteins in the databases are descr 'product' or 'note' qualifiers. Genes that have no signific protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.ht NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Lo http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It shorter because we remove overlaps between neighboring submi
The 5' clone is K8K14 and the 3' clone is LA522.

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BASE COUNT 422 a 265 c 380 g 343 t
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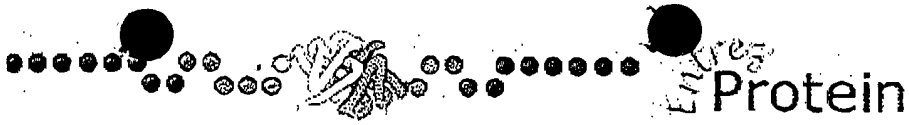

Entrez Protein

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Books

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1: NP_015089. RUVB-like protein... [gi:6325021]

Genome, Nucleotide, Related Sequences, PubMed, Taxonomy, BLink, LinkOut

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LOCUS       NP_015089                471 aa            linear   PLN 03-NOV-2001
DEFINITION  RUVB-like protein, TIP49b Homologue; Rvb2p [Saccharomyces
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ACCESSION   NP_015089
PID         g6325021
VERSION     NP_015089.1  GI:6325021
DBSOURCE    REFSEQ: accession NC_001148.1
KEYWORDS    .
SOURCE      baker's yeast.
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (residues 1 to 471)
  AUTHORS   Goffeau,A., Barrell,B.G., Bussey,H., Davis,R.W., Dujon,B.,
            Feldmann,H., Galibert,F., Hoheisel,J.D., Jacq,C., Johnston,M.,
            Louis,E.J., Mewes,H.W., Murakami,Y., Philippsen,P., Tettelin,H. and
            Oliver,S.G.
  TITLE     Life with 6000 genes
  JOURNAL   Science 274 (5287), 546 (1996)
  MEDLINE   97002444
REFERENCE   2  (residues 1 to 471)
  AUTHORS   Bussey,H., Storms,R.K., Ahmed,A., Albermann,K., Allen,E.,
            Ansorge,W., Araujo,R., Aparicio,A., Barrell,B., Badcock,K.,
            Benes,V., Botstein,D., Bowman,S., Bruckner,M., Carpenter,J.,
            Cherry,J.M., Chung,E., Churcher,C., Coster,F., Davis,K.,
            Davis,R.W., Dietrich,F.S., Delius,H., DiPaolo,T., Hani,J. et al.
  TITLE     The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI
  JOURNAL   Nature 387 (6632 Suppl), 103-105 (1997)
  MEDLINE   97313271
REFERENCE   3  (residues 1 to 471)
  AUTHORS   Saccharomyces Genome Database (yeast-curator@genome.stanford.ed.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-1999) Department of Genetics, Stanford
            University, Saccharomyces Genome Database, Stanford, CA 94305-5120,
            USA
COMMENT     REFSEQ: This reference sequence was provided by the Saccharomyces
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            Method: conceptual translation.
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Revised: October 24, 2001.

1: NP_010476. RUVB-like protein... [gi:6320396]

Genome, Nucleotide, Related Sequences, PubMed, Taxonomy, BLink, LinkOut

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LOCUS       NP_010476                463 aa            linear   PLN 03-NOV-2001
DEFINITION  RUVB-like protein, TIP49a Homologue; Rvb1p [Saccharomyces
            cerevisiae].
ACCESSION   NP_010476
PID         g6320396
VERSION     NP_010476.1  GI:6320396
DBSOURCE    REFSEQ: accession NC_001136.2
KEYWORDS    .
SOURCE      baker's yeast.
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (residues 1 to 463)
  AUTHORS   Goffeau,A., Barrell,B.G., Bussey,H., Davis,R.W., Dujon,B.,
            Feldmann,H., Galibert,F., Hoheisel,J.D., Jacq,C., Johnston,M.,
            Louis,E.J., Mewes,H.W., Murakami,Y., Philippsen,P., Tettelin,H. and
            Oliver,S.G.
  TITLE     Life with 6000 genes
  JOURNAL   Science 274 (5287), 546 (1996)
  MEDLINE   97002444
REFERENCE   2  (residues 1 to 463)
  AUTHORS   Jacq,C., Alt-Morbe,J., Andre,B., Arnold,W., Bahr,A., Ballesta,J.P.,
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            Garcia-Cantalejo,J.M., Goffeau,A., Gomez-Peris,A., Zaccaria,P. et
            al.
  TITLE     The nucleotide sequence of Saccharomyces cerevisiae chromosome IV
  JOURNAL   Nature 387 (6632 Suppl), 75-78 (1997)
  MEDLINE   97313263
REFERENCE   3  (residues 1 to 463)
  AUTHORS   Saccharomyces Genome Database (yeast-curator@genome.stanford.ed.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-1999) Department of Genetics, Stanford
            University, Saccharomyces Genome Database, Stanford, CA 94305-5120,
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      121 lmenfrraig lriketkevy egevteltpe daenplggyg ktishvivgl ksakgtktlr
      181 ldptiyesiq rekvsigdvi yieantgavk rvgrsdayat efdleteeyv plpkgevhkk
      241 keivqdvtlh dldvanarpq ggqdvismmg qllkpkktei teklrqevnk vvakyidqgv
      301 aelipgvlfi devnmldiei ftylnkales niapvvvlas nrgmttvrgt edvisphgvp
      361 pdlidrlliv rtlpydkdei rtiierratv erlqvessal dllatmgtet slryalqlla
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Revised: October 24, 2001.